

PK #10



PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/646,561

DATE: 01/22/2002
TIME: 10:18:17

Input Set : A:\Sequencelisting.txt
Output Set: N:\CRF3\01182002\I646561.raw

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5 <110> APPLICANT: Sim, Gek-Kee
7     Yang, Shumin
9     Sellins, Karen S.
13 <120> TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
15     ACID MOLECULES, AND USES THEREOF
19 <130> FILE REFERENCE: IM-1-C1-PCT
C--> 23 <140> CURRENT APPLICATION NUMBER: US/09/646,561
C--> 25 <141> CURRENT FILING DATE: 2000-09-19
29 <150> PRIOR APPLICATION NUMBER: 60/078,765
31 <151> PRIOR FILING DATE: 1998-03-19
35 <150> PRIOR APPLICATION NUMBER: 09/062,597
37 <151> PRIOR FILING DATE: 1998-04-17
41 <160> NUMBER OF SEQ ID NOS: 65
45 <170> SOFTWARE: PatentIn Ver. 2.0
49 <210> SEQ ID NO: 1
51 <211> LENGTH: 2830
53 <212> TYPE: DNA
55 <213> ORGANISM: Canis familiaris
59 <220> FEATURE:
61 <221> NAME/KEY: CDS
63 <222> LOCATION: (337)..(1248)
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77 gaacatcagc tagatcttcc agcgagtaaa aggaagttgg aaaggggatt gcctctggta 180
81 tatcacccaa agaaaagctg agcaacttgc cattatttg gagacagcaa gaaaggaaca 240
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93
97 tgg aga aca cca cca ctc aaa cac cca tat ctc aag gtc tct cag ctc  402
99 Trp Arg Thr Pro Pro Leu Lys His Pro Tyr Leu Lys Val Ser Gln Leu
101          10          15          20
105 ttg gtg cta gct agt ctc ttt tac ttc tgt tca ggc atc atc cag gtg  450
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109          25          30          35.
113 aac aag aca gtg aaa gaa gta gca gta ctg tcc tgt gat tac aac att  498
115 Asn Lys Thr Val Lys Glu Val Ala Val Leu Ser Cys Asp Tyr Asn Ile
117          40          45          50
121 tcc act aca gaa ctg atg aaa gtt cga atc tat tgg caa aag gat gat  546
123 Ser Thr Thr Glu Leu Met Lys Val Arg Ile Tyr Trp Gln Lys Asp Asp
125          55          60          65          70
129 gaa gtg gtg ctg gct gtc aca tct gga caa acg aaa gtg tgg tcc aag  594

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131	Glu	Val	Val	Leu	Ala	Val	Thr	Ser	Gly	Gln	Thr	Lys	Val	Trp	Ser	Lys	
133							75			80				85			
137	tat	gag	aat	cgc	acc	ttt	gct	gac	ttc	acc	aat	aac	ctc	tcc	atc	gtg	642
139	Tyr	Glu	Asn	Arg	Thr	Phe	Ala	Asp	Phe	Thr	Asn	Asn	Leu	Ser	Ile	Val	
141							90			95				100			
145	att	atg	gct	ctg	cgc	ctg	tca	gac	aat	ggc	aaa	tac	acc	tgt	atc	gtt	690
147	Ile	Met	Ala	Leu	Arg	Leu	Ser	Asp	Asn	Gly	Lys	Tyr	Thr	Cys	Ile	Val	
149							105			110				115			
153	caa	aag	act	gaa	aaa	agg	tct	tac	aaa	gtg	aaa	cac	atg	act	tcg	gtg	738
155	Gln	Lys	Thr	Glu	Lys	Arg	Ser	Tyr	Lys	Val	Lys	His	Met	Thr	Ser	Val	
157							120			125				130			
161	atg	tta	ttg	gtc	aga	gct	gac	ttc	cct	gtc	cct	agt	ata	act	gac	ctt	786
163	Met	Leu	Leu	Val	Arg	Ala	Asp	Phe	Pro	Val	Pro	Ser	Ile	Thr	Asp	Leu	
165	135						140				145			150			
169	gga	aat	cca	tcc	cat	gac	atc	aaa	agg	ata	atg	tgt	tca	acc	tct	gga	834
171	Gly	Asn	Pro	Ser	His	Asp	Ile	Lys	Arg	Ile	Met	Cys	Ser	Thr	Ser	Gly	
173							155			160				165			
177	ggt	ttt	cca	aag	cct	cac	ctc	tcc	tgg	tgg	gaa	aat	gaa	gaa	gaa	ttg	882
179	Gly	Phe	Pro	Lys	Pro	His	Leu	Ser	Trp	Trp	Glu	Asn	Glu	Glu	Glu	Leu	
181							170			175				180			
185	aat	gct	gcc	aac	aca	aca	gtt	tcc	caa	gac	ccg	gac	act	gag	ttg	tac	930
187	Asn	Ala	Ala	Asn	Thr	Thr	Val	Ser	Gln	Asp	Pro	Asp	Thr	Glu	Leu	Tyr	
189							185			190				195			
193	act	att	agt	agt	gaa	ctg	gat	ttc	aat	ata	aca	agc	aac	cat	agc	ttt	978
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201	gtg	tgt	ctt	gtc	aag	tat	gga	gac	tta	aca	gta	tca	cag	atc	ttc	aac	1026
203	Val	Cys	Leu	Val	Lys	Tyr	Gly	Asp	Leu	Thr	Val	Ser	Gln	Ile	Phe	Asn	
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211	Trp	Gln	Lys	Ser	Val	Glu	Pro	His	Pro	Pro	Asn	Asn	Gln	Gln	Gln	Leu	
213							235			240				245			
217	tgg	gtc	atc	ctg	atc	tta	gta	gta	agt	ggt	gtg	att	gct	gtg	atc	act	1122
219	Trp	Val	Ile	Leu	Ile	Leu	Val	Val	Ser	Gly	Val	Ile	Ala	Val	Ile	Thr	
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225	gcc	att	aca	gga	ggc	tgc	cta	gcc	cac	aga	tct	gct	gca	aga	tgg	aga	1170
227	Ala	Ile	Thr	Gly	Gly	Cys	Leu	Ala	His	Arg	Ser	Ala	Ala	Arg	Trp	Arg	
229							265			270				275			
233	cag	aga	aat	agg	aaa	gag	gac	atg	gac	ctg	gaa	aag	atg	tcc	cct		1218
235	Gln	Arg	Asn	Arg	Asn	Lys	Glu	Asp	Met	Asp	Leu	Glu	Lys	Met	Ser	Pro	
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241	ata	aac	ata	gga	tct	gcc	caa	gca	tct	gta	tgaggcagaac	atctggaggt					1268
243	Ile	Asn	Ile	Gly	Ser	Ala	Gln	Ala	Ser	Val							
245	295						300										
249	cccacccca	tcttagattg	acccatctt	tgaatttccct	cagatggcca	ggatttatccc											1328
253	acccatctt	tcatgcattt	gttctctagg	agccgttca	tttcagtgcc	cctgcagaaaa											1388
257	gtgaccagag	gaatatggtg	gggacataag	tagctcttg	gtagccttgg	tcaaagaatt											1448
261	gttcaggcct	gggaagagac	attcgaaaa	tacttgttc	attaatgaca	aggacatcaa											1508
265	ggccttagggg	gtgacctgaa	tgataaaggt	ctgagctaga	acccagattt	cctgtctcgg											1568

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 277 catctgatgc aacactagaa gttttgtgt tgctgtcaaa agcaatctga tgctaattgt 1748
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 285 cagtatctca tcttcattt tggtctcctc tggtcttcc ccacttctcc atcaggttct 1868
 289 ggagaaaagta gatctatcca aaactaatat ctgctgacat gttaagatgaa tgacttataat 1928
 293 acctcaaaagc gatagtcacg ttggagaggg ataggttggt ttagagagtc acatccact 1988
 297 ggttcatatt ggactgataa tctccttaat ggctttatgc tagtttaaac tcatttataa 2048
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 317 tccttcctc gaagttgtct tccataactc agtggaccctg gaggttagacc tgactggagg 2348
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 337 gcatttaatt aaaattaata atccttagac atgctcaaaa ggagacctca agaagtaatc 2648
 341 acaaaaatagg acacatctag gagacagctt atttatactt aaaataaattt atattacatt 2708
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 383 Ser Gly Ile Ile Gln Val Asn Lys Thr Val Lys Glu Val Ala Val Leu
 385 35 40 45
 389 Ser Cys Asp Tyr Asn Ile Ser Thr Thr Glu Leu Met Lys Val Arg Ile
 391 50 55 60
 395 Tyr Trp Gln Lys Asp Asp Glu Val Val Leu Ala Val Thr Ser Gly Gln
 397 65 70 75 80
 401 Thr Lys Val Trp Ser Lys Tyr Glu Asn Arg Thr Phe Ala Asp Phe Thr
 403 85 90 95
 407 Asn Asn Leu Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
 409 100 105 110
 413 Lys Tyr Thr Cys Ile Val Gln Lys Thr Glu Lys Arg Ser Tyr Lys Val
 415 115 120 125
 419 Lys His Met Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val
 421 130 135 140
 425 Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asp Ile Lys Arg Ile
 427 145 150 155 160
 431 Met Cys Ser Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Trp
 433 165 170 175

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449 Thr Ser Asn His Ser Phe Val Cys Leu Val Lys Tyr Gly Asp Leu Thr
451          210           215           220
455 Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Val Glu Pro His Pro Pro
457          225           230           235           240
461 Asn Asn Gln Gln Gln Leu Trp Val Ile Leu Ile Leu Val Val Ser Gly
463          245           250           255
467 Val Ile Ala Val Ile Thr Ala Ile Thr Gly Gly Cys Leu Ala His Arg
469          260           265           270
473 Ser Ala Ala Arg Trp Arg Gln Arg Asn Arg Asn Lys Glu Asp Met Asp
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491 <212> TYPE: DNA

493 <213> ORGANISM: Canis familiaris

497 <400> SEQUENCE: 3

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507 gtaatgtaat ataattttt ttaagtataa ataagctgtc tccttagatgt gtcctatttt 180
511 gtgattactt cttgaggtct cctttgagc atgtctaagg attattaatt ttaattaaat 240
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551 ttttataaaat gagtttaaac tagcataaag ccattaagga gattatcagt ccaatatgaa 840
555 ccagtaggat gtgactctct aaacccaacct atccctctcc aacgtgacta tcgcttttag 900
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603 gacactccag atgttctgct catacagatg cttggcaga tcctatgtt ataggggaca 1620
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VERIFICATION SUMMARY

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L:23 M:270 C: Current Application Number differs, Replaced Current Application Number

L:25 M:271 C: Current Filing Date differs, Replaced Current Filing Date